

L. Specter

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OCT 10 2000

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/236,468A

DATE: 09/22/2000

TIME: 12:39:27

Input Set : A:\Pf201d1.txt

Output Set: N:\CRF3\09222000\I236468A.raw

3 <110> APPLICANT: Soppet et al.
5 <120> TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
7 <130> FILE REFERENCE: PF201D1
9 <140> CURRENT APPLICATION NUMBER: 09/236,468A
10 <141> CURRENT FILING DATE: 1999-01-25
12 <150> PRIOR APPLICATION NUMBER: 08/468,011
13 <151> PRIOR FILING DATE: 1995-06-06
15 <160> NUMBER OF SEQ ID NOS: 28
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2003
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (90)..(1715)
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31 ccctgcttct tcctacagcc gttccgggc atg gcc tgg ctg ggg gcg tcg ctc 113
32 Met Ala Trp Leu Gly Ala Ser Leu
33 1 5
35 cac gtc tgg ggt tgg cta atg ctc gcc agc tgc ctc ctg gcc aga gcc 161
36 His Val Trp Gly Trp Leu Met Leu Gly Ser Cys Leu Leu Ala Arg Ala
37 10 15 20
39 cag ctg gat tct gat gcc acc atc act ata gag gag cag att gtc ctt 209
40 Gln Leu Asp Ser Asp Gly Thr Ile Thr Ile Glu Glu Gln Ile Val Leu
41 25 30 35 40
43 gtg ctg aaa gcg aaa gta caa tgt gaa ctc aac atc aca gct caa ctc 257
44 Val Leu Lys Ala Lys Val Gln Cys Glu Leu Asn Ile Thr Ala Gln Leu
45 45 50 55
47 cag gag gga gaa ggt aat tgt ttc cct gaa tgg gat gga ctc att tgt 305
48 Gln Glu Gly Glu Gly Asn Cys Phe Pro Glu Trp Asp Gly Leu Ile Cys
49 60 65 70
51 tgg ccc aga gga aca gtg ggg aaa ata tcg gct gtt cca tgc cct cct 353
52 Trp Pro Arg Gly Thr Val Gly Lys Ile Ser Ala Val Pro Cys Pro Pro
53 75 80 85
55 tat att tat gac ttc aac cat aaa gga gtt gct ttc cga cac tgt aac 401
56 Tyr Ile Tyr Asp Phe Asn His Lys Gly Val Ala Phe Arg His Cys Asn
57 90 95 100
59 ccc aat gga aca tgg gat ttt atg cac agc tta aat aaa aca tgg gcc 449
60 Pro Asn Gly Thr Trp Asp Phe Met His Ser Leu Asn Lys Thr Trp Ala
61 105 110 115 120
63 aat tat tca gac tgc ctt cgc ttt ctg cag cca gat atc agc ata gga 497
64 Asn Tyr Ser Asp Cys Leu Arg Phe Leu Gln Pro Asp Ile Ser Ile Gly
65 125 130 135
67 aag caa gaa ttc tgt gaa cgc ctc tat gta atg tat acc gtt ggc tac 545
68 Lys Gln Glu Phe Cys Glu Arg Leu Tyr Val Met Tyr Thr Val Gly Tyr

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69          140          145          150
71 tcc atc tct ttt ggt tcc ttg gct gtg gct att ctc atc att ggt tac 593
72 Ser Ile Ser Phe Gly Ser Leu Ala Val Ala Ile Leu Ile Ile Gly Tyr
73          155          160          165
75 ttc aga cga ttg cat tgc act agg aac tat atc cac atg cac tta ttt 641
76 Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Leu Phe
77          170          175          180
79 gtg tct ttc atg ctg aga gct aca agc atc ttt gtc aaa gac aga gta 689
80 Val Ser Phe Met Leu Arg Ala Thr Ser Ile Phe Val Lys Asp Arg Val
81 185          190          195          200
83 gtc cat gct cac ata gga gta aag gag ctg gag tcc cta ata atg cag 737
84 Val His Ala His Ile Gly Val Lys Glu Leu Glu Ser Leu Ile Met Gln
85          205          210          215
87 gat gac cca caa aat tcc att gag gca act tct gtg gac aaa tca caa 785
88 Asp Asp Pro Gln Asn Ser Ile Glu Ala Thr Ser Val Asp Lys Ser Gln
89          220          225          230
91 tat atc ggg tgc aag att gct gtt gtg atg ttt att tac ttc ctg gct 833
92 Tyr Ile Gly Cys Lys Ile Ala Val Val Met Phe Ile Tyr Phe Leu Ala
93          235          240          245
95 aca aat tat tat tgg atc ctg gtg gaa ggt ctc tac ctg cat aat ctc 881
96 Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His Asn Leu
97          250          255          260
99 atc ttt gtg gct ttc ttt tgc gac acc aaa tac ctg tgg ggc ttc atc 929
100 Ile Phe Val Ala Phe Phe Ser Asp Thr Lys Tyr Leu Trp Gly Phe Ile
101 265          270          275          280
103 ttg ata ggc tgg ggg ttt cca gca gca ttt gtt gca gca tgg gct gtg 977
104 Leu Ile Gly Trp Gly Phe Pro Ala Ala Phe Val Ala Ala Trp Ala Val
105          285          290          295
107 gca cga gca act ctg gct gat gcg agg tgc tgg gaa ctt agt gct gga 1025
108 Ala Arg Ala Thr Leu Ala Asp Ala Arg Cys Trp Glu Leu Ser Ala Gly
109          300          305          310
111 gac atc aag tgg att tat caa gca ccg atc tta gca gct att ggg ctg 1073
112 Asp Ile Lys Trp Ile Tyr Gln Ala Pro Ile Leu Ala Ala Ile Gly Leu
113          315          320          325
115 aat ttt att ctg ttt ctg aat acg gtt aga gtt cta gct acc aaa atc 1121
116 Asn Phe Ile Leu Phe Leu Asn Thr Val Arg Val Leu Ala Thr Lys Ile
117          330          335          340
119 tgg gag acc aat gca gtt ggg cat gac aca agg aag caa tac agg aaa 1169
120 Trp Glu Thr Asn Ala Val Gly His Asp Thr Arg Lys Gln Tyr Arg Lys
121 345          350          355          360
123 ctg gcc aaa tgc aca ctg gtc ctg gtc cta gtc ttt gga gtg cat tac 1217
124 Leu Ala Lys Ser Thr Leu Val Leu Val Leu Val Phe Gly Val His Tyr
125          365          370          375
127 atc gtg ttc gtg tgc ctg cct cac tcc ttc act ggg ctc ggg tgg gag 1265
128 Ile Val Phe Val Cys Leu Pro His Ser Phe Thr Gly Leu Gly Trp Glu
129          380          385          390
131 atc cgc atg cac tgt gag ctc ttc ttc aac tcc ttt cag ggt ttc ttt 1313
132 Ile Arg Met His Cys Glu Leu Phe Phe Asn Ser Phe Gln Gly Phe Phe
133          395          400          405

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135 gtg tct atc atc tac tgc tac tgc aat gga gag gtt cag gca gag gtg 1361
136 Val Ser Ile Ile Tyr Cys Tyr Cys Asn Gly Glu Val Gln Ala Glu Val
137 410 415 420
139 aag aag atg tgg agt cgg tgg aat ctc tcc gtg gac tgg aaa agg aca 1409
140 Lys Lys Met Trp Ser Arg Trp Asn Leu Ser Val Asp Trp Lys Arg Thr
141 425 430 435 440
143 ccg cca tgt ggc agc cgc aga tgc ggc tca gtg ctc acc acc gtg acg 1457
144 Pro Pro Cys Gly Ser Arg Arg Cys Gly Ser Val Leu Thr Thr Val Thr
145 445 450 455
147 cac agc acc agc agc cag tca cag gtg gcg gca gca cac gca tgg tgc 1505
148 His Ser Thr Ser Ser Gln Ser Gln Val Ala Ala Ala His Ala Trp Cys
149 460 465 470
151 tta tct ctg gca aag ctg cca aga tcg cca gca gac agc ctg aca gcc 1553
152 Leu Ser Leu Ala Lys Leu Pro Arg Ser Pro Ala Asp Ser Leu Thr Ala
153 475 480 485
155 aca tca ctt tac ctg gct atg tct gga gta act cag agc agg act gcc 1601
156 Thr Ser Leu Tyr Leu Ala Met Ser Gly Val Thr Gln Ser Arg Thr Ala
157 490 495 500
159 tca cac act ctc tcc acg agg agc aac aag gaa gat agt ggg agg cag 1649
160 Ser His Thr Leu Ser Thr Arg Ser Asn Lys Glu Asp Ser Gly Arg Gln
161 505 510 515 520
163 aga gat gat att cta atg gag aag cct tcc agg cct atg gaa tct aac 1697
164 Arg Asp Asp Ile Leu Met Glu Lys Pro Ser Arg Pro Met Glu Ser Asn
165 525 530 535
167 cca gac act gaa gga tgácaaggag aaactgagga tgttctctga atggacatgt 1752
168 Pro Asp Thr Glu Gly
169 540
171 gtggctgact ttcattgggt ggtccaatgg ctggttgtgt gagagggctt ggctgatact 1812
173 cctatgcttg agcacaagg ctgaaaattc agttaaggty ttacttaata atagtttita 1872
175 ggctccatga attggctcct gtaaatacta acgacatgaa aatgcaagt tcaatggagt 1932
177 agttttattac cttctatttg catcaagttt tcctctaaat taatgtatgg tatttgctct 1992
179 gtgattgttc a 2003
182 <210> SEQ ID NO: 2
183 <211> LENGTH: 541
184 <212> TYPE: PRT
185 <213> ORGANISM: Homo sapiens
187 <400> SEQUENCE: 2
188 Met Ala Trp Leu Gly Ala Ser Leu His Val Trp Gly Trp Leu Met Leu
189 1 5 10 15
191 Gly Ser Cys Leu Leu Ala Arg Ala Gln Leu Asp Ser Asp Gly Thr Ile
192 20 25 30
194 Thr Ile Glu Glu Gln Ile Val Leu Val Leu Lys Ala Lys Val Gln Cys
195 35 40 45
197 Glu Leu Asn Ile Thr Ala Gln Leu Gln Glu Gly Glu Gly Asn Cys Phe
198 50 55 60
200 Pro Glu Trp Asp Gly Leu Ile Cys Trp Pro Arg Gly Thr Val Gly Lys
201 65 70 75 80
203 Ile Ser Ala Val Pro Cys Pro Pro Tyr Ile Tyr Asp Phe Asn His Lys
204 85 90 95

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206 Gly Val Ala Phe Arg His Cys Asn Pro Asn Gly Thr Trp Asp Phe Met
207          100          105          110
209 His Ser Leu Asn Lys Thr Trp Ala Asn Tyr Ser Asp Cys Leu Arg Phe
210          115          120          125
212 Leu Gln Pro Asp Ile Ser Ile Gly Lys Gln Glu Phe Cys Glu Arg Leu
213          130          135          140
215 Tyr Val Met Tyr Thr Val Gly Tyr Ser Ile Ser Phe Gly Ser Leu Ala
216 145          150          155          160
218 Val Ala Ile Leu Ile Ile Gly Tyr Phe Arg Arg Leu His Cys Thr Arg
219          165          170          175
221 Asn Tyr Ile His Met His Leu Phe Val Ser Phe Met Leu Arg Ala Thr
222          180          185          190
224 Ser Ile Phe Val Lys Asp Arg Val Val His Ala His Ile Gly Val Lys
225          195          200          205
227 Glu Leu Glu Ser Leu Ile Met Gln Asp Asp Pro Gln Asn Ser Ile Glu
228          210          215          220
230 Ala Thr Ser Val Asp Lys Ser Gln Tyr Ile Gly Cys Lys Ile Ala Val
231 225          230          235          240
233 Val Met Phe Ile Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val
234          245          250          255
236 Glu Gly Leu Tyr Leu His Asn Leu Ile Phe Val Ala Phe Phe Ser Asp
237          260          265          270
239 Thr Lys Tyr Leu Trp Gly Phe Ile Leu Ile Gly Trp Gly Phe Pro Ala
240          275          280          285
242 Ala Phe Val Ala Ala Trp Ala Val Ala Arg Ala Thr Leu Ala Asp Ala
243          290          295          300
245 Arg Cys Trp Glu Leu Ser Ala Gly Asp Ile Lys Trp Ile Tyr Gln Ala
246 305          310          315          320
248 Pro Ile Leu Ala Ala Ile Gly Leu Asn Phe Ile Leu Phe Leu Asn Thr
249          325          330          335
251 Val Arg Val Leu Ala Thr Lys Ile Trp Glu Thr Asn Ala Val Gly His
252          340          345          350
254 Asp Thr Arg Lys Gln Tyr Arg Lys Leu Ala Lys Ser Thr Leu Val Leu
255          355          360          365
257 Val Leu Val Phe Gly Val His Tyr Ile Val Phe Val Cys Leu Pro His
258          370          375          380
260 Ser Phe Thr Gly Leu Gly Trp Glu Ile Arg Met His Cys Glu Leu Phe
261 385          390          395          400
263 Phe Asn Ser Phe Gln Gly Phe Phe Val Ser Ile Ile Tyr Cys Tyr Cys
264          405          410          415
266 Asn Gly Glu Val Gln Ala Glu Val Lys Lys Met Trp Ser Arg Trp Asn
267          420          425          430
269 Leu Ser Val Asp Trp Lys Arg Thr Pro Pro Cys Gly Ser Arg Arg Cys
270          435          440          445
272 Gly Ser Val Leu Thr Thr Val Thr His Ser Thr Ser Ser Gln Ser Gln
273          450          455          460
275 Val Ala Ala Ala His Ala Trp Cys Leu Ser Leu Ala Lys Leu Pro Arg
276 465          470          475          480
278 Ser Pro Ala Asp Ser Leu Thr Ala Thr Ser Leu Tyr Leu Ala Met Ser

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RAW SEQUENCE LISTING DATE: 09/22/2000
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Input Set : A:\Pf201dl.txt
 Output Set: N:\CRF3\09222000\I236468A.raw

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279              485              490              495
281 Gly Val Thr Gln Ser Arg Thr Ala Ser His Thr Leu Ser Thr Arg Ser
282              500              505              510
284 Asn Lys Glu Asp Ser Gly Arg Gln Arg Asp Asp Ile Leu Met Glu Lys
285              515              520              525
287 Pro Ser Arg Pro Met Glu Ser Asn Pro Asp Thr Glu Gly
288              530              535              540
292 <210> SEQ ID NO: 3
293 <211> LENGTH: 23
294 <212> TYPE: DNA
295 <213> ORGANISM: Artificial Sequence
297 <220> FEATURE:
298 <221> NAME/KEY: Primer_Bind
299 <223> OTHER INFORMATION: This 5' primer sequence contains a SmaI restriction
300 enzyme site followed by nucleotides corresponding to PTH receptor
301 coding sequence.
303 <400> SEQUENCE: 3
304 cagccgtccc gggcttgccc tgg                                     23
307 <210> SEQ ID NO: 4
308 <211> LENGTH: 27
309 <212> TYPE: DNA
310 <213> ORGANISM: Artificial Sequence
312 <220> FEATURE:
313 <221> NAME/KEY: Primer_Bind
314 <223> OTHER INFORMATION: This 3' primer sequence contains a SalI restriction
315 enzyme site and a sequence complementary to the human PTH
316 receptor.
318 <400> SEQUENCE: 4
319 cctcagtggtc gacttgatc ccttcag                                     27
322 <210> SEQ ID NO: 5
323 <211> LENGTH: 27
324 <212> TYPE: DNA
325 <213> ORGANISM: Artificial Sequence
327 <220> FEATURE:
328 <221> NAME/KEY: Primer_Bind
329 <223> OTHER INFORMATION: This 5' primer contains a HindIII restriction enzyme site
330 and a nucleotide sequence corresponding to the 5' UTR of the cDNA
331 encoding human PTH receptor.
333 <400> SEQUENCE: 5
334 gttggcatat tggaagcttt ttgcggg                                     27
337 <210> SEQ ID NO: 6
338 <211> LENGTH: 28
339 <212> TYPE: DNA
340 <213> ORGANISM: Artificial Sequence
342 <220> FEATURE:
343 <221> NAME/KEY: Primer_Bind
344 <223> OTHER INFORMATION: This 3' primer sequence contains an XbaI restriction
345 enzyme site, a translation stop codon, and nucleotides
346 complementary to the human PTH receptor coding sequence.

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VERIFICATION SUMMARY

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